



SEQLIST.TXT

SEQUENCE LISTING

<110> Clontech Laboratories Inc.

<120> FAR RED SHIFTED FLUORESCENT PROTEINS

<130> CLON-028WO

<140> Unassigned

<141> 2001-10-12

<150> 60/240,018

<151> 2000-10-12

<150> 60,306,131

<151> 2001-07-16

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<170> FastSEQ for windows Version 4.0

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<211> 910

<212> DNA

<213> heteractis crispa

<400> 1

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ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
gccttcgaca ttttggcacc gtgttgtaga tacggcagca ggaccttgt ccaccatacg 300
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<212> PRT

<213> heteractis crispa

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Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35           40           45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50           55           60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65           70           75           80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
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Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Cys	Thr		
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Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His		
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Lys	Ala	Asn															
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			20					25					30				
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly		
		35					40					45					
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr		
	50				55					60							
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe		
65				70					75					80			
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr		
				85				90					95				
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly		

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Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	Leu	Tyr	Thr	Ser
			165					170						175	
Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe	His
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Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Pro	Arg	Lys	Thr	Lys	Asp	Glu	Tyr
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Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro	Glu
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Lys	Ala	Asn													
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 aagcagtcct tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
 attcttactg ctcatcagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
 gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
 gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
 gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atacttctta caggtccaag 540
 aaagcagtcg gtgccttgac aatgccagga tttcatttta cagacatccg ccttcagatg 600
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<210> 6
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 <213> heteractis crispa

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			20					25					30		
Asn	Pro	Phe	Thr	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu	Gly
		35					40					45			
Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu	Tyr
	50				55					60					
Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe	Phe
65				70					75					80	
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
			85					90					95		
Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu	Gly
		100					105					110			
Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro	Ala
	115					120						125			
Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser	Thr
	130					135					140				
Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val	Met

SEQLIST.TXT

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 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
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 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
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 Lys Ala Asn
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 <213> heteractis crispa

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 tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
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 gtccttggtta ccaattttcc tgctgatggc cccgtgatga agaacaatc aggaggatgg 420
 gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
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 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr

SEQLIST.TXT

195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn
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<213> heteractis crispa

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atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
tggtgtgcgt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
aagcagtcct tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
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gatcttcctg aaaaagcaaa ttga 684

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<213> heteractis crispa

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35 40 45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr
50 55 60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65 70 75 80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100 105 110
Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
115 120 125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130 135 140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145 150 155 160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
165 170 175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180 185 190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
195 200 205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210 215 220
Lys Ala Asn
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SEQLIST.TXT

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 <212> DNA
 <213> heteractis crispa

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 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg His Leu Ile Cys His His Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
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<210> 13
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SEQLIST.TXT

<400> 13

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<210> 14

<211> 227

<212> PRT

<213> heteractis crispa

<400> 14

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Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35      40      45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50      55      60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65      70      75      80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85      90      95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100     105     110
Asn Cys Leu Ile Tyr Lys Val Lys Val His Gly Thr Asn Phe Pro Ala
115     120     125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130     135     140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145     150     155     160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
165     170     175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180     185     190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
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Lys Ala Asn
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<210> 15

<211> 1396

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion construct

<400> 15

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SEQLIST.TXT

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cgcccaccag gacaccagcc tggagggcaa ctgcctgatc tacaaggtga aggtgctggg 1080
caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggct gggagccccag 1140
caccgaggtg gtgtaccccg agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
ggtgggcgac cggcggtcga tctgccacca ctacaccagc taccggagca agaaggccgt 1260
gcgggcccctg accatgcccg gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320
ggagaaggac gagtacttcg agctgtacga ggccagcgtg gcccggtaca gcgacctgcc 1380
cgagaaggcc aactga                                     1396

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<210> 16
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 16

Met	Val	Ser	Gly	Leu	Leu	Lys	Glu	Ser	Met	Arg	Ile	Lys	Met	Tyr	Met
1				5					10					15	
Glu	Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Lys	Cys	Glu	Gly	Glu	Gly	Asp
			20					25					30		
Gly	Asn	Pro	Phe	Ala	Gly	Thr	Gln	Ser	Met	Arg	Ile	His	Val	Thr	Glu
		35					40					45			
Gly	Ala	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ala	Pro	Cys	Cys	Glu
	50				55					60					
Tyr	Gly	Ser	Arg	Thr	Phe	Val	His	His	Thr	Ala	Glu	Ile	Pro	Asp	Phe
65					70				75					80	
Phe	Lys	Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr
			85					90					95		
Tyr	Glu	Asp	Gly	Gly	Ile	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Glu
		100					105					110			
Gly	Asn	Cys	Leu	Ile	Tyr	Lys	Val	Lys	Val	Leu	Gly	Thr	Asn	Phe	Pro
	115					120					125				
Ala	Asp	Gly	Pro	Val	Met	Lys	Asn	Lys	Ser	Gly	Gly	Trp	Glu	Pro	Ser
	130					135				140					
Thr	Glu	Val	Val	Tyr	Pro	Glu	Asn	Gly	Val	Leu	Cys	Gly	Arg	Asn	Val
145					150				155					160	
Met	Ala	Leu	Lys	Val	Gly	Asp	Arg	Arg	Leu	Ile	Cys	His	His	Tyr	Thr
			165					170						175	
Ser	Tyr	Arg	Ser	Lys	Lys	Ala	Val	Arg	Ala	Leu	Thr	Met	Pro	Gly	Phe
		180						185					190		
His	Phe	Thr	Asp	Ile	Arg	Leu	Gln	Met	Leu	Arg	Lys	Glu	Lys	Asp	Glu
	195					200					205				
Tyr	Phe	Glu	Leu	Tyr	Glu	Ala	Ser	Val	Ala	Arg	Tyr	Ser	Asp	Leu	Pro
	210					215				220					
Glu	Lys	Ala	Asn	Arg	Ser	Pro	Gly	Met	Val	Ser	Gly	Leu	Leu	Lys	Glu
225					230				235					240	
Ser	Met	Arg	Ile	Lys	Met	Tyr	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Tyr

SEQLIST.TXT

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                245                250                255
Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
                260                265                270
Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
                275                280                285
Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
                290                295                300
His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
305                310                315
Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
                325                330                335
Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
                340                345                350
Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
                355                360                365
Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
370                375                380
Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
385                390                395
Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
                405                410                415
Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
                420                425                430
Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
                435                440                445
Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn
                450                455                460

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<210> 17
 <211> 1424
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion construct

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<400> 17
accggtcgcc accatggtga gcggcctgct gaaggagagc atgcgcatca agatgtacat 60
ggagggcacc gtgaacggcc actacttcaa gtgcgagggc gagggcgacg gcaacccctt 120
cgccggcacc gagatccatg gcatccacgt gaccgagggc gccccctgac ccttcgcctt 180
cgacatcctg gccccctgct gcgagtacgg cagcaggacc ttcgtgcacc acaccgccga 240
gatccccgac ttcttcaagc agagcttccc cgagggcttc acctgggaga gaaccaccac 300
ctacgaggac ggcgcatcc tgaccgcca ccaggacacc agcctggagg gcaactgcct 360
gatctacaag gtgaaggtgc tgggcaccaa cttccccgcc gacggccccg tgatgaagaa 420
caagagcggc ggctgggagc ccagcaccga ggtggtgtac cccgagaacg gctgctgtg 480
cggccggaac gtgatggccc tgaaggtggg cgaccggcgg ctgatctgcc accactacac 540
cagctaccgg agcaagaagg ccgtgcgggc cctgaccatg cccggcttcc acttcaccga 600
catccggctg cagatgctgc ggaaggagaa ggacgagtac ttcgagctgt acgaggccag 660
cgtggccccg tacagcgacc tgcccagaaa ggccaacaga tctcccggga tggtagcg 720
cctgctgaag gagagcatgc gcatcaagat gtacatggag ggcaccgtga acggccacta 780
cttcaagtgc gagggcgagg gcgacggcaa ccccttcgcc ggcaccaga gcatgcgat 840
ccacgtgacc gagggcgccc ccctgccctt cgcttcgac atcctggccc cctgctgcga 900
gtacggcagc aggaccttcg tgcaccacac cgccgagatc cccgacttct tcaagcagag 960
cttccccgag ggcttcacct gggagagaac caccacctac gaggacggcg gcatcctgac 1020
cgcccaccag gacaccagcc tggagggcaa ctgcctgatc tacaaggtag aggtgctggg 1080
caccaacttc cccgccgacg gccccgtgat gaagaacaag agcggcggct gggagcccag 1140
caccgaggtg gtgtaccccc agaacggcgt gctgtgcggc cggaacgtga tggccctgaa 1200
ggtgggcgac cggcggtga tctgccacca ctaccacagc taccggagca agaaggccgt 1260
gcgggcccctg accatgcccc gcttccactt caccgacatc cggctgcaga tgctgcggaa 1320
ggagaaggac gactacttcg agctgtacga ggccagcgtg gcccgtgata gcgacctgcc 1380
cgagaaggcc aacagaactc gagctatgga tgatgatata gccg 1424

```

SEQLIST.TXT

<210> 18
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct

<400> 18
 Met Val Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met
 1 5 10 15
 Glu Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp
 20 25 30
 Gly Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu
 35 40 45
 Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu
 50 55 60
 Tyr Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe
 65 70 75 80
 Phe Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr
 85 90 95
 Tyr Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu
 100 105 110
 Gly Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro
 115 120 125
 Ala Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser
 130 135 140
 Thr Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val
 145 150 155 160
 Met Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr
 165 170 175 180
 Ser Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe
 185 190 195
 His Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu
 200 205 210
 Tyr Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro
 215 220 225
 Glu Lys Ala Asn Arg Ser Pro Gly Met Val Ser Gly Leu Leu Lys Glu
 230 235 240
 Ser Met Arg Ile Lys Met Tyr Met Glu Gly Thr Val Asn Gly His Tyr
 245 250 255
 Phe Lys Cys Glu Gly Glu Gly Asp Gly Asn Pro Phe Ala Gly Thr Gln
 260 265 270
 Ser Met Arg Ile His Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Phe
 275 280 285
 Asp Ile Leu Ala Pro Cys Cys Glu Tyr Gly Ser Arg Thr Phe Val His
 290 295 300
 His Thr Ala Glu Ile Pro Asp Phe Phe Lys Gln Ser Phe Pro Glu Gly
 305 310 315 320
 Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly Gly Ile Leu Thr
 325 330 335
 Ala His Gln Asp Thr Ser Leu Glu Gly Asn Cys Leu Ile Tyr Lys Val
 340 345 350
 Lys Val Leu Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Asn
 355 360 365
 Lys Ser Gly Gly Trp Glu Pro Ser Thr Glu Val Val Tyr Pro Glu Asn
 370 375 380
 Gly Val Leu Cys Gly Arg Asn Val Met Ala Leu Lys Val Gly Asp Arg
 385 390 395 400
 Arg Leu Ile Cys His His Tyr Thr Ser Tyr Arg Ser Lys Lys Ala Val
 405 410 415
 Arg Ala Leu Thr Met Pro Gly Phe His Phe Thr Asp Ile Arg Leu Gln
 420 425 430

SEQLIST.TXT

Met Leu Arg Lys Glu Lys Asp Glu Tyr Phe Glu Leu Tyr Glu Ala Ser
 435 440 445
 Val Ala Arg Tyr Ser Asp Leu Pro Glu Lys Ala Asn Arg Thr Arg Ala
 450 455 460
 Met Asp Asp Asp Ile Ala
 465 470

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
 acatggatcc gctggtttgt tgaaaga 27

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
 acctcagtgc ttggctccca t 21

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 21
 atgggagcca agcactgagg t 21

<210> 22
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 22
 tgacaagctt ctggtgtcac tggaacaat ca 32

<210> 23
 <211> 684
 <212> DNA
 <213> heteractis crispa

<400> 23
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 ggccattatt tcaagtgtga aggagagggg gacggcaacc catttacagg tacgcagagc 120
 atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat ttggcaccg 180
 tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcctc 240
 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300

SEQLIST.TXT

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attcttactg ctcacacagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
gcccttaaag tcggtgatcg tcgtttgatc tgccatctct atacttctta caggtccaag 540
aaagcagtcc gtgccttgac aatgccagga ttctatttta cagacatccg ctttcagatg 600
ccgaggaaaa agaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
gatcttcctg aaaaagcaaa ttga                                     684

```

<210> 24

<211> 227

<212> PRT

<213> heteractis crispa

<400> 24

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Met Ala Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
1      5      10      15
Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
20     25     30
Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
35     40     45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
50     55     60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
65     70     75     80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85     90     95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
100    105    110
Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
115    120    125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
130    135    140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
145    150    155    160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
165    170    175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
180    185    190
Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Lys Lys Asp Glu Tyr
195    200    205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
210    215    220
Lys Ala Asn
225

```

<210> 25

<211> 683

<212> DNA

<213> heteractis crispa

<400> 25

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atgtctggtt tgttgaaaga aagtatgcgc atcaagatgt acatggaagg cacggttaat 60
ggccattatt tcaagtgtga aggagagggg gacggcaacc catttgacag tacgcagagc 120
atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
tgttgtgcgt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
attcttactg ctcacacagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaaaaatca ggaggatggg 420
agccaagcac tgaggtggtt tatccagaga atggtgtcct gtgtggacgt aatgtgatgg 480
cccttaaagt cgggtgatcg cgtttgatct gccatcacta tacttcttac aggtccaaga 540
aagcagtccg tgccttgaca atgccaggat ttcatattac agacatccgc cttcagatgc 600
tgaggaaaaa gaaagacgag tactttgaac tgtacgaagc atctgtggct aggtacagtg 660

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atcttcctga aaaagcaaatt tga

<210> 26

<211> 227

<212> PRT

<213> heteractis crispa

<400> 26

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Met Ser Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
 1      5      10      15
Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Asp Gly
 20      25      30
Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35      40      45
Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Ala Tyr
 50      55      60
Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65      70      75      80
Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
 85      90      95
Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100     105     110
Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115     120     125
Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
 130     135     140
Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145     150     155     160
Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
 165     170     175
Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180     185     190
Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Lys Lys Asp Glu Tyr
 195     200     205
Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210     215     220
Lys Ala Asn
225

```

<210> 27

<211> 910

<212> DNA

<213> heteractis crispa

<400> 27

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accatttgct ttggttcctt ggcaaacgaa agtttagaac gaaaactgac ccaaattaca 60
tcttcctcct ggatccttac catggctggt ttgttgaaag aaagtatgcg catcaagatg 120
tacatggaag gcacgggttaa tggccattat ttcaagtgtg aaggagaggg agacggcaac 180
ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
gccttcgaca ttttggcacc gtgttgtag tacggcagca ggaccttgt ccaccatacg 300
gcagagattc cggatttctt caagcagtct ttccctgaag gctttacttg ggaaagaacc 360
acaacctatg aagatggagg cattcttact gctcatcagg acacaagcct ggaggggaac 420
tgccttatat acaaggtgaa agtccttggt accaattttc ctgctgatgg ccccgtagtg 480
aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
ctgtgtggac gtaatgtgat ggcccttaaa gtcggtgatc gtcgtttgat ctgccatctc 600
tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
acagacatcc gccttcagat gccgaggaaa acgaaagacg agtactttga actgtacgaa 720
gcactgtggt ctagggtacag tgatcttcct gaaaaagcaa attgattgtt cccagtgaca 780
ccagactgct gtcagctttt ggtaaagcc cgaaagacaa aaggacattt gtagtttagt 840
ttatatttcc ctttcatttg tgaatcaaca ttgtactctc tgtaaaccct taaaatgctc 900
cattaaacct

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SEQLIST.TXT

<210> 28
 <211> 227
 <212> PRT
 <213> heteractis crispa

<400> 28
 Met Ala Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
 1 5 10 15
 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
 20 25 30
 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 35 40 45
 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
 50 55 60
 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr
 85 90 95
 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
 100 105 110
 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Cys Thr
 130 135 140
 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
 145 150 155 160
 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
 165 170 175
 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
 180 185 190
 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
 195 200 205
 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
 210 215 220
 Lys Ala Asn
 225